Please replace the paragraph beginning at page 39, line 17, with the following rewritten paragraph:

A2

--Gene identities were determined by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., *et al.,* (1993) J. Mol. Biol. 215:403-410) searches under default parameters for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm. The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish, W. and States, D. J. (1993) *Nature Genetics 3*:266-272) provided by the NCBI. In some cases, the sequencing data from two or more clones containing overlapping segments of DNA were used to construct contiguous DNA sequences. --

Please replace the paragraph beginning at page 41, line 6, with the following rewritten paragraph:

A3

--ESTs encoding plant transcription factors were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., *et al.*, (1993) *J. Mol. Biol. 215*:403-410) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for

similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish, W. and States, D. J. (1993) *Nature Genetics 3*:266-272 and Altschul, Stephen F., *et al.* (1997) *Nucleic Acids Res. 25*:3389-3402) provided by the NCBI. --

Please replace the paragraph beginning at page 59, line 6, with the following rewritten paragraph:

--The presence of the maize LEC1 polynucleotide was analyzed by PCR using 100-200 ng template DNA in a 30 ml PCR reaction mixture containing 1X concentration enzyme buffer (10 mM Tris-HCl pH 8.8, 1.5 mM magnesium chloride, 50 mM potassium chloride, 0.1% Triton X-100), 200 µM dNTPs, 0.3 µM primers and 0.022 U TaqDNA polymerase (Boehringer Mannheim). Thermocycling conditions were as follows (30 cycles): denaturation at 95°C for 30 s, annealing at 55°C for 1 min and extension at 72°C for 1 min. Primer sequences (F=forward; R=reverse) used were: SEQ ID NO: 25, (F) 5'-CGC TCT GTC ACC TGT TGT ACT C-3', SEQ ID NO: 26, (R) 5'-CGT GAT GAA GCT GAT GTA CTC C-3'. Approximate PCR product length was 620 bp. --

In the Claims:

Please cancel claims 1-3, 13-14, 28, 29, 41, and 42 without prejudice.

Please amend claims 4-5, 9, 11-12, 15, 30-33, 43-45, and 47-49.